In the Specification:

Please replace the paragraph beginning at page 3, line 22, with the following:

--In another aspect, sequences are provided encoding *Lactuca sativa* PAL enzyme and obtainable by polymerase chain reaction of paired degenerate primers GAYCCNYTNAAYTGGGG (SEQ ID NO:6) and CCYTGRAARTTNCCNCCRTG (SEQ ID NO:7).--

Please replace the paragraph beginning at page 4, line 23, with the following:

--Figure 2: Comparison of the conserved regions of several known sequences to PAL (SEQ ID NOS:8-10), from sunflower (HA), *Arabadopsis* (AT), parsley (PC), carrot (DC), tobacco (NT), rice (OS) and wheat (TA), used to design primers for PCR (Genbank accession numbers in parenthesis).--

Please replace the paragraph beginning at page 4, line 29, with the following:

--Figure 4: The cloning strategy adopted to obtain the full-length cDNA. Conserved PAL peptides = SEQ ID NOS:11 and 9.--

Please replace the paragraph beginning at page 6, line 20, with the following:

--Polypeptides of the present invention include isolated polypeptides encoded by a polynucleotide comprising a sequence selected from the group of a sequence contained in Figure 5, and sequences encoding the amino acid sequence of Figure 6 (SEQ ID NOS:3 and 1, respectively). The open reading frame begins at the ATG at base 119, and continues to the stop at 2254.--

Please replace the paragraph beginning at page 8, line 10, with the following:

--The invention also includes polynucleotides of the formula:

$$X\text{-}(R_1)_n\text{-}(R_2)\text{-}(R_3)_n\text{-}Y$$

wherein, at the 5' end, X is hydrogen, and at the 3' end, Y is hydrogen or a metal, R_1 and R_3 are any nucleic acid residue, n is an integer between 1 and 3000, preferably between 1 and 1000 and R_2 is a nucleic acid sequence of the invention, particularly a nucleic acid sequence selected from the sequence of SEQ ID NO:3 and nucleic acid sequences encoding the peptide of SEQ ID NO:1. In the formula, R_2 is oriented so that its 5' end residue is at the left, bound to R_1, and its 3' end residue is at the right, bound to R_3. Any stretch of nucleic acid residues denoted by either R group, where R is greater than 1, may be either a heteropolymer or a homopolymer, preferably a heteropolymer.--

Please replace the paragraph beginning at page 19, line 21, with the following:

--Phenylalanine ammonia-lyase is highly conserved in plants, figure 2, therefore degenerate primers were developed to identify PAL genes in lettuce. As per Figure 2, degenerate primers were designed for polymerase chain reaction (PCR) based on peptide sequences which were similar among sunflower, *Arabidopsis*, parsley, carrot, tobacco, wheat and rice sequences. The peptide sequences chosen for PCR include a region near the 5' end of the PAL encoding sequence, peptide fragment DPLNW (SEQ ID NO:11), and a sequence approximately one-third from the 3' end, encoding the peptide fragment HGGNFQG (SEQ ID NO:9).--

Please replace the paragraph beginning at page 19, line 28, with the following:

--The degenerate primers produced for PCR from these peptide fragments were GAYCCNYTNAAYTGGGG (5') (SEQ ID NO:6) and CCYTGRAARTTNCCNCCRTG (3') (SEQ ID NO:7). These primers were used to PCR

amplify a portion of the open reading frame (ORF) from a *Lactuca sativa* cDNA library. The above primer pairs yielded PCR product which was in the expected range of 1.1 kb (Figure 3). The PCR products were then cloned into a vector which is amplified by expression of the cloned genes in bacteria. Bacterial colonies were selected and checked for the presence of vector insertions. DNA was then purified from the bacterial colonies.--

Please replace the paragraph beginning at page 20, line 22, with the following:

--The methodology used for expression and purification of the fusion protein, MBP-PAL1, in *E. coli* was made following the procedures shown by Nonogaki et al. (2000) with differences explained as follow. Two primers were designed which complement the protein-encoded sequence of LsPAL1. The forward primer (5'-CGGAATTCATGGAGAACGGTAAT-3'; SEQ ID NO:12) included an EcorI site, while the reverse primer (5'-CGTCTAGACTAACATATTGGAAG-3'; SEQ ID NO:13) incorporated an XbaI site. The PAL open reading frame was cloned into the EcorI and XbaI site in pMALc vector (New England Labs, MN). The transformed bacteria were incubated overnight at 37 °C. An aliquot of the overnight culture was used to inoculate an incubation broth for 4 h at 37 °C. The cells were harvested by centrifugation and resuspended in sonication buffer (Nonogaki et al., 2000). After freezing overnight, the cells were thawed and sonicated for 5-10 min to release a higher amount of soluble fusion protein. The soluble protein was purified as Nonogaki et al. (2000) and separated by electrophoresis in a 10% acrylamide gel. The bands were stained with Coomassie brilliant blue (Fisher, PA) for approximately 1 h, and de-stained to visualize the major bands. A pre-stained broad range protein standard (Bio-Rad, CA) was used to estimate the molecular weights.--

Please cancel the "SEQUENCE LISTING", pages 28-39, submitted on December 10, 2001, and insert therefor the accompanying paper copy of the Substitute Sequence